

FIGURE 1

1 AGAAAGGGGT GCGGCAGCAC TGCCAGGGGA AGAGGGTGAT CCGACCCGGG  
51 GAAGGTCGCT GGGCAGGGCG AGTTGGGAAA GCGGCAGCCC CCGCCGCCCC  
101 CGCAGCCCCT TCTCCTCCTT TCTCCACGT CCTATCTGCC TCTCGCTGGA  
151 GGCCAGGCCG TGCAGCATCG AAGACAGGAG GAACTGGAGC CTCATTGGCC  
201 GGCCCGGGGC GCCGGCCTCG GGCTTAAATA GGAGCTCCGG GCTCTGGCTG  
251 GGACCCGACC GCTGCCGGCC GCGCTCCCGC TGCTCCTGCC GGGTGATGGA  
301 AAACCCAGC CCGGCCGCCG CCCTGGGCAA GGCCCTCTGC GCTCTCTCC  
351 TGGCCACTCT CGGCGCCGCC GGCCAGCCTC TTGGGGGAGA GTCCATCTGT  
401 TCCGCCGGAG CCCC GGCCAA ATACAGCATC ACCTTCACGG GCAAGTGGAG  
451 CCAGACGGCC TTCCCAAGC AGTACCCCT GTTCCGCCCC CCTGCGCAGT  
501 GGTCTTCGCT GCTGGGGGCC GCGCATAGCT CCGACTACAG CATGTGGAGG  
551 AAGAACCAGT ACGTCAGTAA CGGGCTGCGC GACTTTGCGG AGCGCGGCGA  
601 GGCCTGGGCG CTGATGAAGG AGATCGAGGC GGCGGGGGAG GCGCTGCAGA  
651 GCGTGACGCG GGTGTTTTTCG GCGCCCGCCG TCCCAGCGG CACCGGGCAG  
701 ACGTCGGCGG AGCTGGAGGT GCAGCGCAGG CACTCGCTGG TCTCGTTTGT  
751 GGTGCGCATC GTGCCCAGCC CCGACTGGTT CGTGGGCGTG GACAGCCTGG  
801 ACCTGTGCGA CGGGGACCGT TGGCGGGAAC AGGCGGCGCT GGACCTGTAC  
851 CCCTACGACG CCGGGACGGA CAGCGGCTTC ACCTTCTCCT CCCCCAATT  
901 CGCCACCATC CCGCAGGACA CGGTGACCGA GATAACGTCC TCCTCTCCCA  
951 GCCACCCGGC CAACTCCTTC TACTACCCAC GGCTGAAGGC CCTGCCTCCC  
1001 ATCGCCAGGG TGACACTGGT GCGGCTGCGA CAGAGCCCCA GGGCCTTCAT  
1051 CCCTCCCGCC CCAGTCCTGC CCAGCAGGGA CAATGAGATT GTAGACAGCG  
1101 CCTCAGTTCC AGAAACGCCG CTGGACTGCG AGGTCTCCCT GTGGTCGTCC  
1151 TGGGGACTGT GCGGAGGCCA CTGTGGGAGG CTCGGGACCA AGAGCAGGAC  
1201 TCGCTACGTC CGGGTCCAGC CCGCCAACAA CGGGAGCCCC TGCCCCGAGC  
1251 TCGAAGAAGA GGCTGAGTGC GTCCCTGATA ACTGCGTCTA AGACCAGAGC

FIGURE 1- continued

1301 CCCGCAGCCC CTGGGGCCCC CCGGAGCCAT GGGGTGTCGG GGGCTCCTGT  
1351 GCAGGCTCAT GCTGCAGGCG GCCGAGGGCA CAGGGGGTTT CGCGCTGCTC  
1401 CTGACCGCGG TGAGGCCGCG CCGACCATCT CTGCACTGAA GGGCCCTCTG  
1451 GTGGCCGGCA CGGGCATTGG GAAACAGCCT CCTCCTTTCC CAACCTTGCT  
1501 TCTTAGGGGC CCCCGTGTCC CGTCTGCTCT CAGCCTCCTC CTCCTGCAGG  
1551 ATAAAGTCAT CCCCAAGGCT CCAGCTACTC TAAATTATGT CTCCTTATAA  
1601 GTTATTGCTG CTCCAGGAGA TTGTCCTTCA TCGTCCAGGG GCCTGGCTCC  
1651 CACGTGGTTG CAGATACCTC AGACCTGGTG CTCTAGGCTG TGCTGAGCCC  
1701 ACTCTCCCGA GGGCGCATCC AAGCGGGGGC CACTTGAGAA GTGAATAAAT  
1751 GGGGCGGTTT CGGAAGCGTC AAAAAAAAAA AAAAA

## FIGURE 2

1 MENPSPAAAL GKALCALLLA TLGAAGQPLG GESICSAGAP AKYSITFTGK  
51 WSOTAFPKOY PLFRPPAOWS SLIGAHHSSD YSMWRKNOYV SNGLRDFAER  
101 GEAWALMKEI EAAGEALQSV HAVFSAPAVP SGTGQTSDEL EVORRHSLVS  
151 FYVRIVPSPD WFGYDSLDEL CDGDRWREOA ALDLYPYDAG TDSGFTESSP  
201 NEATIPODTY TEITSSSPSH PANSFYYPRL KALPPIARVT LVRLRQSPRA  
251 FIPPAPVLPS RDNEIVDSAS VPETPLDCEV SLWSSWGLCG GHCGRIGTKS  
301 RTRYVRVQPA NNGSPCPELE EEAECVPDNC V

# FIGURE 3

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RG1      1 MENPSPAAALGKALCALLLATLGA.AGQPLGGESICSAGAPAKYSITFTG 49
      ||| | .| : | ||| ||. ||||| |||:|. | |:|||||
mindin 1 MENVS..FSLDRTLWVFLLAMLGSTAGQPLGGESVCTARPLARYSITFTG 48

      50 KWSQTAFPKQYPLFRPPAQWSSLLGAAHSSDYSMWKRKNQYVSNGLRDFAE 99
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      49 KWSQTAFPKQYPLFRPPAQWSSLLGAAHSSDYSMWKRKNEYVSNGLRDFAE 98

      100 RGEAWALMKEIEAAGEALQSVHAVFSAPAVPSGTGQTSAELEVQRRHSLV 149
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      99 RGEAWALMKEIEAAGEKLQSVHAVFSAPAVPSGTGQTSAELEVHPRHSLV 148

      150 SFVVRIVPSPDWFVGVDSLDLCDGDRWREQAALDLYPYDAGTDSGFTFSS 199
      ||||| ||||| |||||:|||||:| ||:| |||||:||||| |||||
      149 SFVVRIVPSPDWFVGIDSLDLCEGGRWKEQVVL DLYPHDAGTDSGFTFSS 198

      200 PNFATIPQDTVTEITSSSPSHPANSFYYPRLKALPPIARVTLVRLRQSPR 249
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      199 PNFATIPQDTVTEITASSPSHPANSFYYPRLKSLPPIAKVTFVRLRQSPR 248

      250 AFIPPAPVLP SRDNEIVDSASVPETPLDCEVSLWSSWGLCGGHCGR LGTK 299
      || ||. | || ||||| ||||| ||||| ||||| ||||| |||||
      249 AFAPPSLDLASRGNEIVDSL SVPETPLDCEVSLWSSWGLCGGPCGKL GAK 298

      300 SRTRYVRVQPANNGSPCPELEEEAECPDNCV 331
      ||||| ||||| ||||| ||||| |||||
      299 SRTRYVRVQPANNGTPCPELEEEAECPDNCV 330

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FIGURE 4

1 AGAAAGGGGTGCGGCAGCACTGCCAGGGGAAGAGGGTGATCCGACCCGGGGAAGGTCGCT 60  
 TCTTTCCCCACGCCGTCGTGACGGTCCCCTTCTCCCACTAGGCTGGGCCCCCTTCCAGCGA  
 GGGCAGGGCGAGTTGGGAAAGCGGCAGCCCCCGCGCCCCCGCAGCCCCCTTCTCCTCCTT  
 61 120  
 CCCGTCCCGCTCAACCCCTTTCGCCGTCGGGGGCGGCGGGGGCGTCGGGGAAGAGGAGGAA  
 TCTCCACGTCCTATCTGCCTCTCGCTGGAGGCCAGGCCGTGCAGCATCGAAGACAGGAG  
 121 180  
 AGAGGGTGCAGGATAGACGGAGAGCGACCTCCGGTCCGGCACGTCGTAGCTTCTGTCTC  
 GAACTGGAGCCTCATTGGCCGGCCCCGGGGCGCGGCCTCGGGCTTAAATAGGAGCTCCGG  
 181 240  
 CTTGACCTCGGAGTAACCGGCCGGCCCCCGCGGCCGAGCCCGAATTTATCCTCGAGGCC  
 GCTCTGGCTGGGACCCGACCGCTGCCGGCCGCGCTCCCGCTGCTCCTGCCGGGTGATGGA  
 241 300  
 CGAGACCGACCTGGGCTGGCGACGGCCGGCGAGGGCGACGAGGACGGCCCACTACCT  
 b M E -  
 301 AAACCCAGCCCGGCCGCGCCCTGGGCAAGGCCCTCTGCGCTCTCCTCCTGGCCACTCT  
 TTTGGGGTCGGGCCGGCGCGGGACCCGTTCCGGGAGACGCGAGAGGAGGACCGGTGAGA  
 b N P S P A A A L G K A L C A L L L A T L -  
 361 CGGCGCCGCCGGCCAGCCTCTTGGGGGAGAGTCCATCTGTTCCGCCGGAGCCCCGGCCAA  
 GCCGCGCGGCCGGTCCGGAACCCCTCTCAGGTAGACAAGGCGGCCCTCGGGGCCGGTT  
 b G A A G Q P L G G E S I C S A G A P A K -  
 421 ATACAGCATCACCTTCACGGGCAAGTGGAGCCAGACGGCCTTCCCCAAGCAGTACCCCT  
 TATGTCGTAGTGAAGTGCCCGTTCACCTCGGTCTGCCGAAGGGGTTCTGTCATGGGGGA  
 b Y S I T F T G K W S Q T A F P K Q Y P L -  
 481 GTTCCGCCCCCTGCGCAGTGGTCTTCTGCTGCTGGGGGCGCGCATAGCTCCGACTACAG  
 CAAGCGGGGGGACGCGTCACCAAGAAGCGACGACCCCGCGCGTATCGAGGCTGATGTC  
 b F R P P A Q W S S L L G A A H S S D Y S -  
 541 CATGTGGAGGAAGAACCAGTACGTACGTACAGTAACGGGCTGCGCGACTTTGCGGAGCGCGCGA  
 GTACACCTCCTTCTTGGTCATGCAGTCATTGCCCGACGCGCTGAAACGCTCGCGCCGCT  
 b M W R K N Q Y V S N G L R D F A E R G E -  
 601 GGCCTGGGCGCTGATGAAGGAGATCGAGGCGGGGGGGAGGCGCTGCAGAGCGTGCACGC  
 CCGGACCCGCGACTACTTCTCTAGCTCCGCGCCCCCTCCGCGACGTCTCGCACGTGCG  
 b A W A L M K E I E A A G E A L Q S V H A -  
 661 GGTGTTTTTCGGCGCCCGCGTCCCCAGCGGACCGGGCAGACGTCGGCGGAGCTGGAGGT  
 CCACAAAAGCCGCGGGCGGCAGGGGTGCGCGTGGCCCGTCTGCAGCCGCTCGACCTCCA  
 b V F S A P A V P S G T G Q T S A E L E V -

FIGURE 4 - continued

CGAGCGCAGGCACTCGCTGGTCTCGTTTGTGGTGCGCATCGTGCCCAGCCCCGACTGGTT  
 721 -----+-----+-----+-----+-----+-----+-----+ 780  
 CGTCGCGTCCGTGAGCGACCAGAGCAAACACCACGCGTAGCACGGGTCGGGGCTGACCAA  
 b       Q R R H S L V S F V V R I V P S P D W F -  
 CGTGGGCGTGGACAGCCTGGACCTGTGCGACGGGACCGTTGGCGGGAACAGGCGGCGCT  
 781 -----+-----+-----+-----+-----+-----+-----+ 840  
 GCACCCGCACCTGTGCGACCTGGACACGCTGCCCTGGCAACCGCCCTTGTCCGCGCGA  
 b       V G V D S L D L C D G D R W R E Q A A L -  
 GGACCTGTACCCCTACGACGCCGGGACGGACAGCGGCTTACCTTCTCCTCCCCCACTT  
 841 -----+-----+-----+-----+-----+-----+-----+ 900  
 CCTGGACATGGGGATGCTGCGGCCCTGCCTGTGCGCGAAGTGAAGAGGAGGGGGTTGAA  
 b       D L Y P Y D A G T D S G F T F S S P N F -  
 CGCCACCATCCCGCAGGACACGGTGACCGAGATAACGTCCTCCTCTCCAGCCACCCGGC  
 901 -----+-----+-----+-----+-----+-----+-----+ 960  
 GCGGTGGTAGGGCGTCTGTGCCACTGGCTCTATTGCAGGAGGAGAGGGTCGGTGGGCCG  
 b       A T I P Q D T V T E I T S S S P S H P A -  
 CAACTCCTTCTACTACCCACGGCTGAAGGCCCTGCCTCCCATCGCCAGGGTGACACTGGT  
 961 -----+-----+-----+-----+-----+-----+-----+ 1020  
 GTTGAGGAAGATGATGGGTGCCGACTTCCGGGACGGAGGGTAGCGGTCCCACTGTGACCA  
 b       N S F Y Y P R L K A L P P I A R V T L V -  
 GCGGCTGCGACAGAGCCCCAGGGCCTTCATCCCTCCCGCCCCAGTCCTGCCCAGCAGGGA  
 1021 -----+-----+-----+-----+-----+-----+-----+ 1080  
 CGCCGACGCTGTCTCGGGGTCCCGGAAGTAGGGAGGGCGGGGTCAGGACGGGTCTGTCCT  
 b       R L R Q S P R A F I P P A P V L P S R D -  
 CAATGAGATTGTAGACAGCGCCTCAGTTCCAGAAACGCCGCTGGACTGCGAGGTCTCCCT  
 1081 -----+-----+-----+-----+-----+-----+-----+ 1140  
 GTTACTCTAACATCTGTGCGGAGTCAAGGTCTTTGCGGCGACCTGACGCTCCAGAGGGA  
 b       N E I V D S A S V P E T P L D C E V S L -  
 GTGGTCTGCTGGGACTGTGCGGAGGCCACTGTGGGAGGCTCGGGACCAAGAGCAGGAC  
 1141 -----+-----+-----+-----+-----+-----+-----+ 1200  
 CACCAGCAGGACCCCTGACACGCCTCCGGTGACACCCTCCGAGCCCTGGTTCTCGTCTG  
 b       W S S W G L C G G H C G R L G T K S R T -  
 TCGCTACGTCCGGGTCCAGCCCCCAACAACGGGAGCCCCCTGCCCGAGCTCGAAGAAGA  
 1201 -----+-----+-----+-----+-----+-----+-----+ 1260  
 AGCGATGCAGGCCAGGTGCGGGCGTTGTTGCCCTCGGGGACGGGCTCGAGCTTCTTCT  
 b       R Y V R V Q P A N N G S P C P E L E E E -  
 GGCTGAGTGGTCCCTGATAACTGCGTCTAAGACCAGAGCCCCGAGCCCCCTGGGGCCCC  
 1261 -----+-----+-----+-----+-----+-----+-----+ 1320  
 CCGACTCACGCAGGGACTATTGACGCAGATTCTGGTCTCGGGGCGTCGGGGACCCCGGG  
 b       A E C V P D N C V \*  
 CCGGAGCCATGGGGTGTGCGGGGCTCCTGTGCAGGCTCATGCTGCAGGCGGCCGAGGGCA  
 1321 -----+-----+-----+-----+-----+-----+-----+ 1380  
 GGCCTCGGTACCCACAGCCCCCGAGGACACGTCCGAGTACGACGTCCGCCGGCTCCCGT  
 CAGGGGGTTTCGCGCTGCTCCTGACCGCGGTGAGGCCGCGCCGACCATCTCTGCACTGAA  
 1381 -----+-----+-----+-----+-----+-----+-----+ 1440  
 GTCCCCCAAAGCGGACGAGGACTGGCGGCACTCCGGCGCGGCTGGTAGAGACGTGACTT  
 GGGCCCTCTGGTGGCCGGCACGGGCATTGGGAAACAGCCTCCTCCTTTCCCAACCTTGCT  
 1441 -----+-----+-----+-----+-----+-----+-----+ 1500  
 CCCGGGAGACCACCGGCCGTGCCCGTAACCTTTGTGCGAGGAGGAAAGGGTTGGAACGA

# FIGURE 4 - continued

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1501 TCTTAGGGGCCCCCGTGTCCCGTCTGCTCTCAGCCTCCTCCTCCTGCAGGATAAAGTCAT
-----+-----+-----+-----+-----+-----+ 1560
AGAATCCCCGGGGGCACAGGGCAGACGAGAGTCGGAGGAGGAGGACGTCCTATTTTCAGTA

CCCCAAGGCTCCAGCTACTCTAAATTATGTCTCCTTATAAGTTATTGCTGCTCCAGGAGA
1561 -----+-----+-----+-----+-----+-----+ 1620
GGGGTTCCGAGGTCGATGAGATTTAATACAGAGGAATATTCAATAACGACGAGGTCCTCT

TTGTCCTTCATCGTCCAGGGGCTGGCTCCACGTGGTTGCAGATACCTCAGACCTGGTG
1621 -----+-----+-----+-----+-----+-----+ 1680
AACAGGAAGTAGCAGGTCCCCGGACCGAGGGTGCACCAACGTCTATGGAGTCTGGACCAC

CTCTAGGCTGTGCTGAGCCCACTCTCCCGAGGGCGCATCCAAGCGGGGGCCACTTGAGAA
1681 -----+-----+-----+-----+-----+-----+ 1740
GAGATCCGACACGACTCGGGTGAGAGGGCTCCCGCGTAGGTCGCCCCCGGTGAACTCTT

GTGAATAAATGGGGCGGTTTCGGAAGCGTC
1741 -----+-----+-----+ 1770
CACTTATTTACCCCGCCAAAGCCTTCGCAG

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FIGURE 5

Expression of *Rg1* mRNA in human tissues

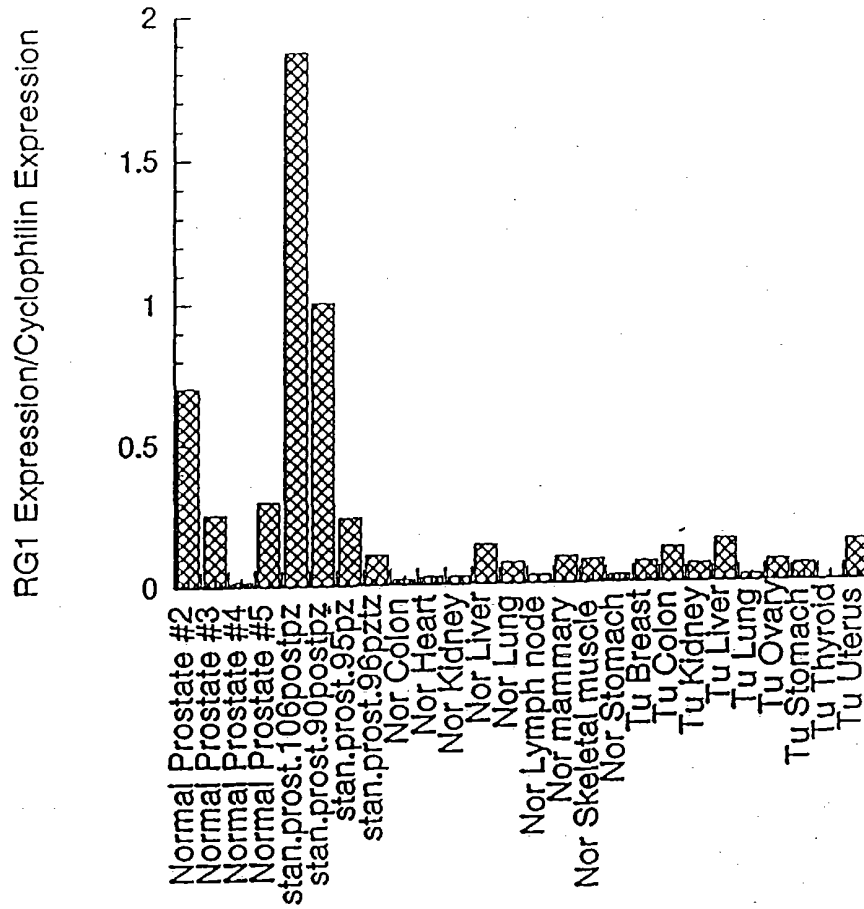
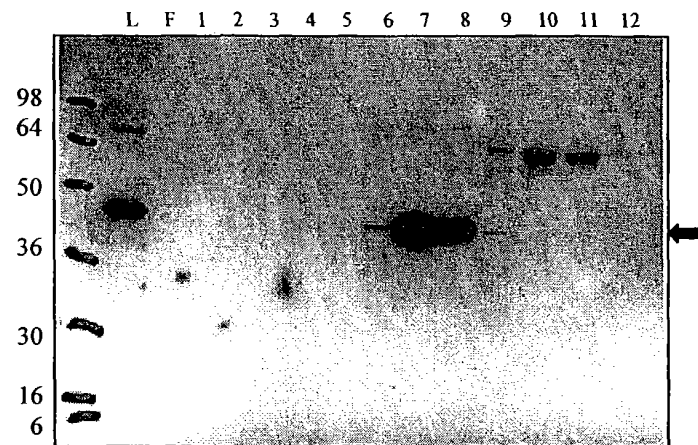




FIGURE 6

Purification of Native RG1 Protein Secreted  
by LNCaP Cells.



**FIGURE 7**  
Immunohistochemical staining of RG1 expression

